

BC

#6



PCT10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/031,355

DATE: 06/12/2002

TIME: 12:05:28

Input Set : A:\PU3513USw Seq Listing.txt

Output Set: N:\CRF3\06122002\J031355.raw

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3 <110> APPLICANT: Glaxo Group Limited
4      Knick, Vincent C
5      Stimmel, Julie B
6      Thurmond, Linda M
8 <120> TITLE OF INVENTION: Antibody combination
10 <130> FILE REFERENCE: PU3513
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/031,355
C--> 13 <141> CURRENT FILING DATE: 2002-05-15
18 <160> NUMBER OF SEQ ID NOS: 16
20 <170> SOFTWARE: PatentIn Ver.. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 740
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (24)..(740)
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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37      Met Gly Trp Ser Cys Ile Ile Leu Phe Leu
38      1 5 10
40 gta gca aca gct aca ggt gtc cac tcc gat att gtg atg act cag tct 101
41 Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Val Met Thr Gln Ser
42      15 20 25
44 cca ctc tcc ctg ccc gtc acc cct gga gag ccg gcc tcc atc tcc tgt 149
45 Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys
46      30 35 40
48 agg tct agt aag aat ctc ctg cat agt aat ggc atc act tat ttg tat 197
49 Arg Ser Ser Lys Asn Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr
50      45 50 55
52 tgg tac ctg cag aag cca ggg cag tct cca cag ctc ctg atc tat cag 245
53 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln
54      60 65 70
56 atg tcc aac ctt gcc tca ggg gtc cct gac agg ttc agt agc agt gga 293
57 Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly
58 75 80 85 90
60 tca ggc aca gat ttt aca ctg aaa atc agc aga gtg gag gct gag gat 341
61 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
62      95 100 105
64 gtt ggg gtt tat tac tgt gct caa aat cta gag att cct cgg acg ttc 389

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65 Val Gly Val Tyr Tyr Cys Ala Gln Asn Leu Glu Ile Pro Arg Thr Phe
66      110      115      120
68 ggc caa ggg acc aag gtg gag atc aaa cgt acg gtg gct gca cca tct 437
69 Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
70      125      130      135
72 gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc 485
73 Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
74      140      145      150
77 tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta 533
78 Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
79 155      160      165      170
81 cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt 581
82 Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
83      175      180      185
85 gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc 629
86 Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
87      190      195      200
89 ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc 677
90 Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
91      205      210      215
93 gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac 725
94 Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
95      220      225      230
97 agg gga gag tgt tag 740
98 Arg Gly Glu Cys
99 235
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 238
104 <212> TYPE: PRT
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
109 sequence
111 <400> SEQUENCE: 2
112 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
113 1 5 10 15
115 Val His Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
116 20 25 30
118 Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Asn Leu
119 35 40 45
121 Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro
122 50 55 60
124 Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser
125 65 70 75 80
127 Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr
128 85 90 95
130 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
131 100 105 110
133 Ala Gln Asn Leu Glu Ile Pro Arg Thr Phe Gly Gln Gly Thr Lys Val

```

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134          115          120          125
136 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
137          130          135          140
139 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
140 145          150          155          160
142 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
143          165          170          175
145 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
146          180          185          190
148 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
149          195          200          205
151 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
152          210          215          220
154 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
155 225          230          235

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159 &lt;210&gt; SEQ ID NO: 3

160 &lt;211&gt; LENGTH: 740

161 &lt;212&gt; TYPE: DNA

162 &lt;213&gt; ORGANISM: Artificial Sequence

164 &lt;220&gt; FEATURE:

165 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
166 sequence

168 &lt;400&gt; SEQUENCE: 3

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169 ctaacactct cccctgttga agctctttgt gacgggagcag ctcaggccct gatgggtgac 60
170 ttcgcaggcg tagactttgt gtttctcgta gtctgctttg ctcagcgta ggggtgctgct 120
171 gaggtgtag gtgtgtctct tgtgtctctg ctctgtgaca ctctcctggg agttaccgca 180
172 ttggaggggc ttatccacct tccactgtac tttggcctct ctgggataga agttattcag 240
173 caggcacaca acagaggcag ttccagattt caactgctca tcagatggcg ggaagatgaa 300
174 gacagatggt gcagccaccg tacgtttgat ctccaccttg gtcccttggc cgaacgtccg 360
175 aggaatctct agattttgag cacagtaata aacccaaca tcctcagcct cactctgct 420
176 gattttcagt gtaaaatctg tgcctgatcc actgctactg aacctgtcag ggaccctga 480
177 ggcaagggtt gacatctgat agatcaggag ctgtggagac tgccctggct tctgcaggta 540
178 ccaatacaaa taagtgatgc cattactatg caggagattc ttactagacc tacaggagat 600
179 ggaggccggc tctccagggg tgacgggcag ggagagtgga gactgagtca tcacaatatc 660
180 ggagtggaca cctgtagctg ttgctaccaa gaagaggatg atacagctcc atcccatggt 720
181 gaggtcctgt gaagcttacg                                     740

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184 &lt;210&gt; SEQ ID NO: 4

185 &lt;211&gt; LENGTH: 1418

186 &lt;212&gt; TYPE: DNA

187 &lt;213&gt; ORGANISM: Artificial Sequence

189 &lt;220&gt; FEATURE:

190 &lt;221&gt; NAME/KEY: CDS

191 &lt;222&gt; LOCATION: (24)..(1418)

194 &lt;220&gt; FEATURE:

195 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
196 sequence

198 &lt;400&gt; SEQUENCE: 4

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199 cgtaagcttc acagatcctc acc atg gga tgg agc tgt atc atc ctc ttt ctg 53
200 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu

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201							1			5				10			
203	gtg	gca	aca	gct	aca	ggg	gtc	cac	tcc	cag	gta	cag	cta	gtg	caa	tca	101
204	Val	Ala	Thr	Ala	Thr	Gly	Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	
205						15				20					25		
207	ggg	cct	gaa	gtg	aag	aag	cct	ggg	gcc	tca	gtg	aaa	gtt	tcc	tgc	aag	149
208	Gly	Pro	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	
209				30				35					40				
211	gct	tct	ggc	tac	acc	ttc	acc	aac	tat	gga	atg	aac	tgg	gta	agg	cag	197
212	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	
213			45					50					55				
215	gcg	cct	gga	cag	ggg	ctt	gag	tgg	atg	ggg	tgg	ata	aac	acc	tac	act	245
216	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	
217		60					65					70					
219	gga	gag	cca	aca	tat	ggg	gaa	gat	ttc	aag	gga	cgg	ttt	gca	ttc	tct	293
220	Gly	Glu	Pro	Thr	Tyr	Gly	Glu	Asp	Phe	Lys	Gly	Arg	Phe	Ala	Phe	Ser	
221	75					80				85					90		
223	cta	gac	aca	tcc	gcc	agc	aca	gcc	tat	atg	gag	ctc	agc	tcg	ctg	aga	341
224	Leu	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	
225				95						100					105		
227	tcc	gag	gac	act	gca	gtc	tat	ttc	tgt	gcg	aga	ttt	ggg	aac	tac	gta	389
228	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Asn	Tyr	Val	
229			110					115					120				
232	gac	tac	tgg	ggg	caa	gga	tca	cta	gtc	act	gtc	tcc	tca	gcc	tcc	acc	437
233	Asp	Tyr	Trp	Gly	Gln	Gly	Ser	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	
234			125				130					135					
236	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	485
237	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	
238		140				145					150						
240	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	533
241	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	
242	155				160				165					170			
244	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	581
245	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	
246			175					180					185				
248	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	629
249	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	
250			190					195					200				
252	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	677
253	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	
254		205					210					215					
256	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	725
257	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	
258		220				225					230						
260	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	773
261	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
262	235				240				245					250			
264	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	821
265	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	
266			255					260					265				

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269 gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      869
270 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
271                               270                               275           280
273 gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      917
274 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
275                               285                               290           295
277 ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac      965
278 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
279                               300                               305           310
281 aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac      1013
282 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
283 315                               320                               325           330
285 tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc      1061
286 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
287                               335                               340           345
289 cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga      1109
290 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
291                               350                               355           360
293 gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag      1157
294 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
295                               365                               370           375
297 aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac      1205
298 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
299                               380                               385           390
301 atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag      1253
302 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
303 395                               400                               405           410
306 acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc      1301
307 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
308                               415                               420           425
310 aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca      1349
311 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
312                               430                               435           440
314 tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc      1397
315 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
316                               445                               450           455
318 ctc tcc ctg tct ccg ggt aaa                                      1418
319 Leu Ser Leu Ser Pro Gly Lys
320                               460                               465
323 <210> SEQ ID NO: 5
324 <211> LENGTH: 465
325 <212> TYPE: PRT
326 <213> ORGANISM: Artificial Sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
330 sequence
332 <400> SEQUENCE: 5
333 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
334 1 5 10 15

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/031,355

DATE: 06/12/2002

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Input Set : A:\PU3513USw Seq Listing.txt

Output Set: N:\CRF3\06122002\J031355.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date